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#2

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/084,843

DATE: 03/12/2002
TIME: 09:41:42

Input Set : N:\Crf3\RULE60\10084843.raw
Output Set: N:\CRF3\03122002\J084843.raw

SEQUENCE LISTING
3 (1) GENERAL INFORMATION:
5   (i) APPLICANT: Reed, Steven G.
6   Skeiky, Yasir A.W.
7   Dillon, Davin C.
8   Campos-Neto, Antonio
9   Houghton, Raymond
10   Vedvick, Thomas S.
11   Twardzik, Daniel R.
12   Lodes, Michael J.
13   Hendrickson, Ronald C.
15   (ii) TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
16   AND DIAGNOSIS OF TUBERCULOSIS
18   (iii) NUMBER OF SEQUENCES: 355
20   (iv) CORRESPONDENCE ADDRESS:
21   (A) ADDRESSEE: SEED and BERRY LLP
22   (B) STREET: 6300 Columbia Center, 701 Fifth Avenue
23   (C) CITY: Seattle
24   (D) STATE: Washington
25   (E) COUNTRY: USA
26   (F) ZIP: 98104-7092
28   (v) COMPUTER READABLE FORM:
29   (A) MEDIUM TYPE: Floppy disk
30   (B) COMPUTER: IBM PC compatible
31   (C) OPERATING SYSTEM: PC-DOS/MS-DOS
32   (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
34   (vi) CURRENT APPLICATION DATA:
C--> 35   (A) APPLICATION NUMBER: US/10/084,843
C--> 36   (B) FILING DATE: 25-Feb-2002
37   (C) CLASSIFICATION:
39   (vii) PRIOR APPLICATION DATA:
40   (A) APPLICATION NUMBER: US/09/072,967
41   (B) FILING DATE: 05-MAY-1998
44   (viii) ATTORNEY/AGENT INFORMATION:
45   (A) NAME: Maki, David J.
46   (B) REGISTRATION NUMBER: 31,392
47   (C) REFERENCE/DOCKET NUMBER: 210121.411C9
49   (ix) TELECOMMUNICATION INFORMATION:
50   (A) TELEPHONE: (206) 622-4900
51   (B) TELEFAX: (206) 682-6031
54 (2) INFORMATION FOR SEQ ID NO: 1:
56   (i) SEQUENCE CHARACTERISTICS:
57   (A) LENGTH: 766 base pairs

RAW SEQUENCE LISTING   DATE: 03/12/2002
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Input Set : **N:\Crf3\RULE60\10084843.raw**
Output Set: **N:\CRF3\03122002\J084843.raw**

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58                (B) TYPE: nucleic acid
59                (C) STRANDEDNESS: single
60                (D) TOPOLOGY: linear
62      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
64 CGAGGCACCG GTAGTTTGAA CCAAACGCAC AATCGACGGG CAAACGAACG GAAGAACACA        60
65 ACCATGAAGA TGGTGAAATC GATCGCCGCA GGTCTGACCG CCGCGGCTGC AATCGGCGCC       120
66 GCTGCGGCCG GTGTGACTTC GATCATGGCT GGCGGCCCGG TCGTATACCA GATGCAGCCG       180
67 GTCGTCTTCG GCGCGCCACT GCCGTTGGAC CCGGCATCCG CCCCTGACGT CCCGACCGCC       240
68 GCCCAGTTGA CCAGCCTGCT CAACAGCCTC GCCGATCCCA ACGTGTCGTT TGCGAACAAG       300
69 GGCAGTCTGG TCGAGGGCGG CATCGGGGGC ACCGAGGCGC GCATCGCCGA CCACAAGCTG       360
70 AAGAAGGCCG CCGAGCACGG GGATCTGCCG CTGTCGTTCA GCGTGACGAA CATCCAGCCG       420
71 GCGGCCGCCG GTTCGGCCAC CGCCGACGTT TCCGTCTCGG GTCCGAAGCT CTCGTCGCCG       480
72 GTCACGCAGA ACGTCACGTT CGTGAATCAA GGCGGCTGGA TGCTGTCACG CGCATCGGCG       540
73 ATGGAGTTGC TGCAGGCCGC AGGGNAACTG ATTGGCGGGC CGGNTTCAGC CCGCTGTTCA       600
74 GCTACGCCGC CCGCCTGGTG ACGCGTCCAT GTCGAACACT CGCGCGTGTA GCACGGTGCG       660
75 GTNTGCGCAG GGNCGCACGC ACCGCCCGGT GCAAGCCGTC CTCGAGATAG GTGGTGNCTC       720
76 GNCACCAGNG ANCACCCCCN NNTCGNCNNT TCTCGNTGNT GNATGA                     766
78 (2) INFORMATION FOR SEQ ID NO: 2:
80      (i) SEQUENCE CHARACTERISTICS:
81                (A) LENGTH: 752 base pairs
82                (B) TYPE: nucleic acid
83                (C) STRANDEDNESS: single
84                (D) TOPOLOGY: linear
86      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
88 ATGCATCACC ATCACCATCA CGATGAAGTC ACGGTAGAGA CGACCTCCGT CTTCCGCGCA        60
89 GACTTCCTCA GCGAGCTGGA CGCTCCTGCG CAAGCGGGTA CGGAGAGCGC GGTCTCCGGG       120
90 GTGGAAGGGC TCCCGCCGGG CTCGGCGTTG CTGGTAGTCA AACGAGGCCC CAACGCCGGG       180
91 TCCCGGTTCC TACTCGACCA AGCCATCACG TCGGCTGGTC GGCATCCCGA CAGCGACATA       240
92 TTTCTCGACG ACGTGACCGT GAGCCGTCGC CATGCTGAAT TCCGGTTGGA AAACAACGAA       300
93 TTCAATGTCG TCGATGTCGG GAGTCTCAAC GGCACCTACG TCAACCGCGA GCCCGTGGAT       360
94 TCGGCGGTGC TGGCGAACGG CGACGAGGTC CAGATCGGCA AGCTCCGGTT GGTGTTCTTG       420
95 ACCGGACCCA AGCAAGGCGA GGATGACGGG AGTACCGGGG GCCCGTGAGC GCACCCGATA       480
96 GCCCCGCGCT GGCCGGGATG TCGATCGGGG CGGTCCTCCG ACCTGCTACG ACCGGATTTT       540
97 CCCTGATGTC CACCATCTCC AAGATTCGAT TCTTGGGAGG CTTGAGGGTC NGGGTGACCC       600
98 CCCCGCGGGC CTCATTCNGG GGTNTCGGCN GGTTTCACCC CNTACCNACT GCCNCCCGGN       660
99 TTGCNAATTC NTTCTTCNCT GCCCNNAAAG GGACCNTTAN CTTGCCGCTN GAAANGGTNA       720
100 TCCNGGGCCC NTCCTNGAAN CCCCNTCCCC CT                                    752
102 (2) INFORMATION FOR SEQ ID NO: 3:
104     (i) SEQUENCE CHARACTERISTICS:
105               (A) LENGTH: 813 base pairs
106               (B) TYPE: nucleic acid
107               (C) STRANDEDNESS: single
108               (D) TOPOLOGY: linear
110     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
112 CATATGCATC ACCATCACCA TCACACTTCT AACCGCCCAG CGCGTCGGGG GCGTCGAGCA        60
113 CCACGCGACA CCGGGCCCGA TCGATCTGCT AGCTTGAGTC TGGTCAGGCA TCGTCGTCAG       120
114 CAGCGCGATG CCCTATGTTT GTCGTCGACT CAGATATCGC GGCAATCCAA TCTCCCGCCT       180
115 GCGGCCGGCG GTGCTGCAAA CTACTCCCGG AGGAATTTCG ACGTGCGCAT CAAGATCTTC       240
116 ATGCTGGTCA CGGCTGTCGT TTTGCTCTGT TGTTCGGGTG TGGCCACGGC CGCGCCCAAG       300
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117 ACCTACTGCG AGGAGTTGAA AGGCACCGAT ACCGGCCAGG CGTGCCAGAT TCAAATGTCC        360
118 GACCCGGCCT ACAACATCAA CATCAGCCTG CCCAGTTACT ACCCCGACCA GAAGTCGCTG        420
119 GAAAATTACA TCGCCCAGAC GCGCGACAAG TTCCTCAGCG CGGCCACATC GTCCACTCCA        480
120 CGCGAAGCCC CCTACGAATT GAATATCACC TCGGCCACAT ACCAGTCCGC GATACCGCCG        540
121 CGTGGTACGC AGGCCGTGGT GCTCAMGGTC TACCACAACG CCGGCGGCAC GCACCCAACG        600
122 ACCACGTACA AGGCCTTCGA TTGGGACCAG GCCTATCGCA AGCCAATCAC CTATGACACG        660
123 CTGTGGCAGG CTGACACCGA TCCGCTGCCA GTCGTCTTCC CCATTGTTGC AAGGTGAACT        720
124 GAGCAACGCA GACCGGGACA ACWGGTATCG ATAGCCGCCN AATGCCGGCT TGGAACCCNG        780
125 TGAAATTATC ACAACTTCGC AGTCACNAAA NAA                                      813
127 (2) INFORMATION FOR SEQ ID NO: 4:
129     (i) SEQUENCE CHARACTERISTICS:
130         (A) LENGTH: 447 base pairs
131         (B) TYPE: nucleic acid
132         (C) STRANDEDNESS: single
133         (D) TOPOLOGY: linear
135     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
137 CGGTATGAAC ACGGCCGCGT CCGATAACTT CCAGCTGTCC CAGGGTGGGC AGGGATTCGC         60
138 CATTCCGATC GGGCAGGCGA TGGCGATCGC GGGCCAGATC CGATCGGGTG GGGGGTCACC        120
139 CACCGTTCAT ATCGGGCCTA CCGCCTTCCT CGGCTTGGGT GTTGTCGACA ACAACGGCAA        180
140 CGGCGCACGA GTCCAACGCG TGGTCGGGAG CGCTCCGGCG GCAAGTCTCG GCATCTCCAC        240
141 CGGCGACGTG ATCACCGCGG TCGACGGCGC TCCGATCAAC TCGGCCACCG CGATGGCGGA        300
142 CGCGCTTAAC GGGCATCATC CCGGTGACGT CATCTCGGTG AACTGGCAAA CCAAGTCGGG        360
143 CGGCACGCGT ACAGGGAACG TGACATTGGC CGAGGGACCC CCGGCCTGAT TTCGTCGYGG        420
144 ATACCACCCG CCGGCCGGCC AATTGGA                                            447
146 (2) INFORMATION FOR SEQ ID NO: 5:
148     (i) SEQUENCE CHARACTERISTICS:
149         (A) LENGTH: 604 base pairs
150         (B) TYPE: nucleic acid
151         (C) STRANDEDNESS: single
152         (D) TOPOLOGY: linear
154     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
156 GTCCCACTGC GGTCGCCGAG TATGTCGCCC AGCAAATGTC TGGCAGCCGC CCAACGGAAT         60
157 CCGGTGATCC GACGTCGCAG GTTGTCGAAC CCGCCGCCGC GGAAGTATCG GTCCATGCCT        120
158 AGCCCGGCGA CGGCGAGCGC CGGAATGGCG CGAGTGAGGA GGCGGGCAAT TTGGCGGGGC        180
159 CCGGCGACGG NGAGCGCCGG AATGGCGCGA GTGAGGAGGT GGNCAGTCAT GCCCAGNGTG        240
160 ATCCAATCAA CCTGNATTCG GNCTGNGGGN CCATTTGACA ATCGAGGTAG TGAGCGCAAA        300
161 TGAATGATGG AAAACGGGNG GNGACGTCCG NTGTTCTGGT GGTGNTAGGT GNCTGNCTGG        360
162 NGTNGNGGNT ATCAGGATGT TCTTCGNCGA AANCTGATGN CGAGGAACAG GGTGTNCCCG        420
163 NNANNCCNAN GGNGTCCNAN CCCNNNNTCC TCGNCGANAT CANANAGNCG NTTGATGNGA        480
164 NAAAAGGGTG GANCAGNNNN AANTNGNGGN CCNAANAANC NNNANNGNNG NNAGNTNGNT        540
165 NNNTNTTNNC ANNNNNNNTG NNGNNGNNCN NNNCAANCNN NTNNNNGNAA NNGGNTTNTT        600
166 NAAT                                                                     604
168 (2) INFORMATION FOR SEQ ID NO: 6:
170     (i) SEQUENCE CHARACTERISTICS:
171         (A) LENGTH: 633 base pairs
172         (B) TYPE: nucleic acid
173         (C) STRANDEDNESS: single
174         (D) TOPOLOGY: linear
176     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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178 TTGCANGTCG AACCACCTCA CTAAAGGGAA CAAAAGCTNG AGCTCCACCG CGGTGGCGGC      60
179 CGCTCTAGAA CTAGTGKATM YYYCKGGCTG CAGSAATYCG GYACGAGCAT TAGGACAGTC     120
180 TAACGGTCCT GTTACGGTGA TCGAATGACC GACGACATCC TGCTGATCGA CACCGACGAA     180
181 CGGGTGCGAA CCCTCACCCT CAACCGGCCG CAGTCCCGYA ACGCGCTCTC GGCGGCGCTA     240
182 CGGGATCGGT TTTTCGCGGY GTTGGYCGAC GCCGAGGYCG ACGACGACAT CGACGTCGTC     300
183 ATCCTCACCG GYGCCGATCC GGTGTTCTGC GCCGGACTGG ACCTCAAGGT AGCTGGCCGG     360
184 GCAGACCGCG CTGCCGGACA TCTCACCGCG GTGGGCGGCC ATGACCAAGC CGGTGATCGG     420
185 CGCGATCAAC GGCGCCGCGG TCACCGGCGG GCTCGAACTG GCGCTGTACT GCGACATCCT     480
186 GATCGCCTCC GAGCACGCCC GCTTCGNCGA CACCCACGCC CGGGTGGGGC TGCTGCCCAC     540
187 CTGGGGACTC AGTGTGTGCT TGCCGCAAAA GGTCGGCATC GGNCTGGGCC GGTGGATGAG     600
188 CCTGACCGGC GACTACCTGT CCGTGACCGA CGC                                  633
190 (2) INFORMATION FOR SEQ ID NO: 7:
192      (i) SEQUENCE CHARACTERISTICS:
193           (A) LENGTH: 1362 base pairs
194           (B) TYPE: nucleic acid
195           (C) STRANDEDNESS: single
196           (D) TOPOLOGY: linear
198      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
200 CGACGACGAC GGCGCCGGAG AGCGGGCGCG AACGGCGATC GACGCGGCCC TGGCCAGAGT      60
201 CGGCACCACC CAGGAGGGAG TCGAATCATG AAATTTGTCA ACCATATTGA GCCCGTCGCG     120
202 CCCCGCCGAG CCGGCGGCGC GGTCGCCGAG GTCTATGCCG AGGCCCGCCG CGAGTTCGGC     180
203 CGGCTGCCCG AGCCGCTCGC CATGCTGTCC CCGGACGAGG GACTGCTCAC CGCCGGCTGG     240
204 GCGACGTTGC GCGAGACACT GCTGGTGGGC CAGGTGCCGC GTGGCCGCAA GGAAGCCGTC     300
205 GCCGCCGCCG TCGCGGCCAG CCTGCGCTGC CCCTGGTGCG TCGACGCACA CACCACCATG     360
206 CTGTACGCGG CAGGCCAAAC CGACACCGCC GCGGCGATCT TGGCCGGCAC AGCACCTGCC     420
207 GCCGGTGACC CGAACGCGCC GTATGTGGCG TGGGCGGCAG GAACCGGGAC ACCGGCGGGA     480
208 CCGCCGGCAC CGTTCGGCCC GGATGTCGCC GCCGAATACC TGGGCACCGC GGTGCAATTC    .540
209 CACTTCATCG CACGCCTGGT CCTGGTGCTG CTGGACGAAA CCTTCCTGCC GGGGGGCCCG     600
210 CGCGCCCAAC AGCTCATGCG CCGCGCCGGT GGACTGGTGT TCGCCCGCAA GGTGCGCGCG     660
211 GAGCATCGGC CGGGCCGCTC CACCCGCCGG CTCGAGCCGC GAACGCTGCC CGACGATCTG     720
212 GCATGGGCAA CACCGTCCGA GCCCATAGCA ACCGCGTTCG CCGCGCTCAG CCACCACCTG     780
213 GACACCGCGC CGCACCTGCC GCCACCGACT CGTCAGGTGG TCAGGCGGGT CGTGGGGTCG     840
214 TGGCACGGCG AGCCAATGCC GATGAGCAGT CGCTGGACGA ACGAGCACAC CGCCGAGCTG     900
215 CCCGCCGACC TGCACGCGCC CACCCGTCTT GCCCTGCTGA CCGGCCTGGC CCCGCATCAG     960
216 GTGACCGACG ACGACGTCGC CGCGGCCCGA TCCCTGCTCG ACACCGATGC GGCGCTGGTT    1020
217 GGCGCCCTGG CCTGGGCCGC CTTCACCGCC GCGCGGCGCA TCGGCACCTG GATCGGCGCC    1080
218 GCCGCCGAGG GCCAGGTGTC GCGGCAAAAC CCGACTGGGT GAGTGTGCGC GCCCTGTCGG    1140
219 TAGGGTGTCA TCGCTGGCCC GAGGGATCTC GCGGCGGCGA ACGGAGGTGG CGACACAGGT    1200
220 GGAAGCTGCG CCCACTGGCT TGCGCCCCAA CGCCGTCGTG GGCGTTCGGT TGGCCGCACT    1260
221 GGCCGATCAG GTCGGCGCCG GCCCTTGGCC GAAGGTCCAG CTCAACGTGC CGTCACCGAA    1320
222 GGACCGGACG GTCACCGGGG GTCACCCTGC GCGCCCAAGG AA                       1362
224 (2) INFORMATION FOR SEQ ID NO: 8:
226      (i) SEQUENCE CHARACTERISTICS:
227           (A) LENGTH: 1458 base pairs
228           (B) TYPE: nucleic acid
229           (C) STRANDEDNESS: single
230           (D) TOPOLOGY: linear
232      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
234 GCGACGACCC CGATATGCCG GGCACCGTAG CGAAAGCCGT CGCCGACGCA CTCGGGCGCG      60
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Input Set : **N:\Crf3\RULE60\10084843.raw**
Output Set: **N:\CRF3\03122002\J084843.raw**

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235 GTATCGCTCC CGTTGAGGAC ATTCAGGACT GCGTGGAGGC CCGGCTGGGG GAAGCCGGTC    120
236 TGGATGACGT GGCCCGTGTT TACATCATCT ACCGGCAGCG GCGCGCCGAG CTGCGGACGG    180
237 CTAAGGCCTT GCTCGGCGTG CGGGACGAGT TAAAGCTGAG CTTGGCGGCC GTGACGGTAC    240
238 TGCGCGAGCG CTATCTGCTG CACGACGAGC AGGGCCGGCC GGCCGAGTCG ACCGGCGAGC    300
239 TGATGGACCG ATCGGCGCGC TGTGTCGCGG CGGCCGAGGA CCAGTATGAG CCGGGCTCGT    360
240 CGAGGCGGTG GGCCGAGCGG TTCGCCACGC TATTACGCAA CCTGGAATTC CTGCCGAATT    420
241 CGCCCACGTT GATGAACTCT GGCACCGACC TGGGACTGCT CGCCGGCTGT TTTGTTCTGC    480
242 CGATTGAGGA TTCGCTGCAA TCGATCTTTG CGACGCTGGG ACAGGCCGCC GAGCTGCAGC    540
243 GGGCTGGAGG CGGCACCGGA TATGCGTTCA GCCACCTGCG ACCCGCCGGG GATCGGGTGG    600
244 CCTCCACGGG CGGCACGGCC AGCGGACCGG TGTCGTTTCT ACGGCTGTAT GACAGTGCCG    660
245 CGGGTGTGGT CTCCATGGGC GGTCGCCGGC GTGGCGCCTG TATGGCTGTG CTTGATGTGT    720
246 CGCACCCGGA TATCTGTGAT TTCGTCACCG CCAAGGCCGA ATCCCCCAGC GAGCTCCCGC    780
247 ATTTCAACCT ATCGGTTGGT GTGACCGACG CGTTCCTGCG GGCCGTCGAA CGCAACGGCC    840
248 TACACCGGCT GGTCAATCCG CGAACCGGCA AGATCGTCGC GCGGATGCCC GCCGCCGAGC    900
249 TGTTCGACGC CATCTGCAAA GCCGCGCACG CCGGTGGCGA TCCCGGGCTG GTGTTTCTCG    960
250 ACACGATCAA TAGGGCAAAC CCGGTGCCGG GGAGAGGCCG CATCGAGGCG ACCAACCCGT   1020
251 GCGGGGAGGT CCCACTGCTG CCTTACGAGT CATGTAATCT CGGCTCGATC AACCTCGCCC   1080
252 GGATGCTCGC CGACGGTCGC GTCGACTGGG ACCGGCTCGA GGAGGTCGCC GGTGTGGCGG   1140
253 TGCGGTTCCT TGATGACGTC ATCGATGTCA GCCGCTACCC CTTCCCCGAA CTGGGTGAGG   1200
254 CGGCCCGCGC CACCCGCAAG ATCGGGCTGG GAGTCATGGG TTTGGCGGAA CTGCTTGCCG   1260
255 CACTGGGTAT TCCGTACGAC AGTGAAGAAG CCGTGCGGTT AGCCACCCGG CTCATGCGTC   1320
256 GCATACAGCA GGCGGCGCAC ACGGCATCGC GGAGGCTGGC CGAAGAGCGG GGCGCATTCC   1380
257 CGGCGTTCAC CGATAGCCGG TTCGCGCGGT CGGGCCCGAG GCGCAACGCA CAGGTCACCT   1440
258 CCGTCGCTCC GACGGGCA                                                 1458
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260 (2) INFORMATION FOR SEQ ID NO: 9:
262   (i) SEQUENCE CHARACTERISTICS:
263   (A) LENGTH: 862 base pairs
264   (B) TYPE: nucleic acid
265   (C) STRANDEDNESS: single
266   (D) TOPOLOGY: linear
268   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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270 ACGGTGTAAT CGTGCTGGAT CTGGAACCGC GTGGCCCGCT ACCTACCGAG ATCTACTGGC     60
271 GGCGCAGGGG GCTGGCCCTG GGCATCGCGG TCGTCGTAGT CGGGATCGCG GTGGCCATCG    120
272 TCATCGCCTT CGTCGACAGC AGCGCCGGTG CCAAACCGGT CAGCGCCGAC AAGCCGGCCT    180
273 CCGCCCAGAG CCATCCGGGC TCGCCGGCAC CCCAAGCACC CCAGCCGGCC GGGCAAACCG    240
274 AAGGTAACGC CGCCGCGGCC CCGCCGCAGG GCCAAAACCC CGAGACACCC ACGCCCACCG    300
275 CCGCGGTGCA GCCGCCGCCG GTGCTCAAGG AAGGGGACGA TTGCCCCGAT TCGACGCTGG    360
276 CCGTCAAAGG TTTGACCAAC GCGCCGCAGT ACTACGTCGG CGACCAGCCG AAGTTCACCA    420
277 TGGTGGTCAC CAACATCGGC CTGGTGTCCT GTAAACGCGA CGTTGGGGCC GCGGTGTTGG    480
278 CCGCCTACGT TTACTCGCTG GACAACAAGC GGTTGTGGTC CAACCTGGAC TGCGCGCCCT    540
279 CGAATGAGAC GCTGGTCAAG ACGTTTTCCC CCGGTGAGCA GGTAACGACC GCGGTGACCT    600
280 GGACCGGGAT GGGATCGGCG CCGCGCTGCC CATTGCCGCG GCCGGCGATC GGGCCGGGCA    660
281 CCTACAATCT CGTGGTACAA CTGGGCAATC TGCGCTCGCT GCCGGTTCCG TTCATCCTGA    720
282 ATCAGCCGCC GCCGCCGCCC GGGCCGGTAC CCGCTCCGGG TCCAGCGCAG GCGCCTCCGC    780
283 CGGAGTCTCC CGCGCAAGGC GGATAATTAT TGATCGCTGA TGGTCGATTC CGCCAGCTGT    840
284 GACAACCCCT CGCCTCGTGC CG                                             862
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286 (2) INFORMATION FOR SEQ ID NO: 10:
288   (i) SEQUENCE CHARACTERISTICS:
289   (A) LENGTH: 622 base pairs

VERIFICATION SUMMARY DATE: 03/12/2002
PATENT APPLICATION: **US/10/084,843** TIME: 09:41:43

Input Set : **N:\Crf3\RULE60\10084843.raw**
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L:36 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:1269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:1325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
L:1338 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59
L:1365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
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L:1481 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65
L:1535 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67
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L:3651 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:124
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L:3693 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:127
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L:3755 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:131
L:3772 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:132
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L:3798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:134
L:3811 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:135
L:3837 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137
L:4152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:145
L:4164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:145
L:10862 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:343
L:10864 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:343
L:10879 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:344
L:10894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:345
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VERIFICATION SUMMARY
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L:10909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:346
L:10924 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:347
L:10926 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:347
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